

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 13:00:25 ; Search time 30 seconds
(without alignments)
570.805 Million cell updates/sec

Title: US-09-635-949-34
Perfect score: 3289
Sequence: 1 MDPILLALVSSILQAAK.....TGFICLDVSLKHCSEER 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1092.5	33.2	553	4	US-09-249-697A-6
2	1092.5	33.2	553	4	US-09-363-316B-6
3	1091.5	33.2	553	4	US-09-249-697A-19
4	1091.5	33.2	553	4	US-09-363-316B-24
5	1041.5	31.7	502	4	US-09-363-316B-18
6	1041.5	31.7	537	4	US-09-249-697A-4
7	1041.5	31.7	537	4	US-09-363-316B-4
8	594	18.1	164	4	US-09-249-697A-9
9	594	18.1	164	4	US-09-363-316B-9
10	409.5	12.5	100	4	US-09-249-697A-3
11	409.5	12.5	100	4	US-09-363-316B-3
12	353.5	10.7	443	4	US-08-833-963C-2
13	353.5	10.7	443	3	US-08-980-514-1
14	327	9.9	638	2	US-08-897-443-1
15	327	9.9	835	4	US-09-284-819-6
16	326.5	9.9	448	2	US-08-884-072-1
17	326.5	9.9	448	4	US-09-212-168-1
18	323	9.8	652	2	US-08-751-305-2
19	322.5	9.8	956	2	US-08-697-443-3
20	317	9.6	1833	3	US-08-479-722B-2
21	317	9.6	1833	5	PCT-US95-02251-18
22	314.5	9.6	2556	1	US-08-185-432-17
23	314.5	9.6	2556	1	US-08-083-590A-20
24	314.5	9.6	2556	3	US-08-532-384-20
25	314.5	9.6	2556	4	US-08-899-232-2
26	310.5	9.4	2523	1	US-08-185-432-18
27	310.5	9.4	2523	4	US-08-899-232-3

28	307.5	9.3	337	4	US-09-188-930-186	Sequence 186, Appl
29	295.5	9.0	1394	6	5177197-30	Patent No. 5177197
30	295	9.0	387	2	US-08-884-072-5	Sequence 5, Appl1
31	295	9.0	387	2	US-08-833-963C-9	Sequence 9, Appl1
32	295	9.0	387	3	US-08-980-514-3	Sequence 3, Appl1
33	295	9.0	387	4	US-09-212-168-5	Sequence 5, Appl1
34	290.5	8.8	1964	4	US-09-467-997-1	Sequence 1, Appl1
35	285	8.7	1253	3	US-08-479-722H-4	Sequence 4, Appl1
36	283	8.6	1251	5	PCT-US95-02251-3	Sequence 3, Appl1
37	283	8.6	1252	1	US-08-199-780-3	Sequence 3, Appl1
38	283	8.6	1252	2	US-08-316-650-3	Sequence 3, Appl1
39	282	8.6	274	4	US-09-188-930-336	Sequence 336, App
40	280.5	8.5	728	4	US-08-981-392-2	Sequence 2, Appl1
41	280.5	8.5	1148	4	US-08-882-046-4	Sequence 4, Appl1
42	278	8.5	1219	4	US-08-882-046-5	Sequence 5, Appl1
43	276.5	8.4	1238	4	US-09-214-278-5	Sequence 5, Appl1
44	275.5	8.4	810	2	US-08-820-170A-34	Sequence 34, Appl1
45	275.5	8.4	810	3	US-09-055-699-34	Sequence 34, Appl1

ALIGNMENTS

RESULT 1
US-09-249-697A-6
; Sequence 6, Application US/09249697A
; Patent No. 6392018
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL LIVER SPLEEN
; FILE REFERENCE: 24011-727
; CURRENT APPLICATION NUMBER: US/09/249,697A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(553)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-6

Query Match	33.2%	Score	1092.5	DB	4	Length	553
Best Local Similarity	37.7%	Pred. No.	3.3e-68				
Matches	215	Conservative	96	Mismatches	173	Indels	87
Gaps	14						
QY	34	GLCRYGGRIDCGWARGSGCOPFYVLRQRIARICQIKAVCCPRCKHGECIGNCKK	93				
Db	39	GVCYGTLCACCYGRRNSKGVCE-----ATCPGCKPFGCVGNCKR	81				
QY	94	CHPGVAGTKICQVLNECGLKPRCKHRCMNTYGSYKCYCLNGYMLMPDGSCSALTCSMA	153				
Db	82	CFPGYTGKTCSDVDNCCGKMPKPCOHRVNTGSKYKCLSGHMLPDIATCVNSRTCAMI	141				
QY	154	NCQYQCDVVVKGIQRCOTSPGLQAPDGTQVDVDFCATGRASCPKPCOCVNIPOSYICK	213				
Db	142	NCQYSCDTEEGPQCLCPSSGLRLAPNGRDCIDIDECASGKVICPYNRRCVNTFGSYCK	201				
QY	214	CHKGFPLMVGKYCHDIDECISLGOYQCSSFARCVNPGSYKCKKCYOGELTCVYI	273				
Db	202	CHIGFELVIGRYDCIDINECTMDSHTCSHANCNTQCSFKCKCKCYKONGKLCSAI	261				
QY	274	PKVMTEPSGPIVKGNGTILKGTGNNWIPDVSGTWPPKTPYIPPIITNRPSTKPTT	333				
Db	262	PNNSVK-----EVLKAPGTH-----KDRIKKILAHKNSMKKA	294				

QY 435 LVHSCNFDHGLCQWIREKNDLHWEP1-RDPAGGYLTVSAAKAPGGAARLVLPGLRLM 493
DB 399 SV-DCSFNHCIDKQDREDDFDWADPDRDNAIGFYMAVPALAGHKDIGRLKLLPDQ 457
QY 494 HSGDCLSLFRHKVTGLHSGTLOVFRKKAHCAALWGRNGHG--WROQTITL-RCAD-I 549
DB 458 POSNFCLLFDYRLAGDKVCKLRFVFK--NSNNALAWKTTSEDEKWKTKIOLYQGTDTAT 515
QY 550 KSVVFKEKRRGHTGEIGLDDVSLKKGHCSE 580
DB 516 KSLIFEAEKRGKTKGTAIVDGVLLVSGICPD 546
RESULT 4
US-09-363-316B-24
; Sequence 24, Application US/093633116B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-363-316B-24

Query Match 33.2%; Score 1091.5; DB 4; Length 553;
Best Local Similarity 37.7%; Pred. No. 3.9e-68;
Matches 215; Conservative 96; Mismatches 173; Indels 87; Gaps 14;
QY 34 GICRYGGRIDCCMGARQSGOCOPFYVLRQRIARCQLKAVCPCKKHGBCIGNKCK 93
DB 39 GVCHYGTKLACCYGWRNSKVC-----ATCEPCCKFGEVCGVGNKCR 81
QY 94 CHPGYAGKTCIQVLEGLKPRCKHRCMNTGYSKYCLNGYMLMPOGSSSALTCSMA 153
DB 82 CFPYTGKTCSDQVNECGMKPRPCQHRVCNTHGSKYKFCCLSGHMLMPDTCVNSRTCAMI 141
QY 154 NCOYGCDDVVKGOIRCOCPSPGLQAPDGRTCVDVDECATGRASCPFRFCVNTFGSYCK 213
DB 142 NCOYSCDETEEGPQCLPSSGURLAPNGRDCLDIDECASGKVICPYNRRVCNTEFGSYCK 201
QY 214 CHKGFDLMYTCCQYCHDIDKCSIGQYQCSFARCYNVRGSKYCKCKEYQGGDGLTCVY 273
DB 202 CHIGFELQYISGRYDCIDINECTMDSHTCSHHANCNTQGSFKCKCKQYKGNGLRCSAI 261
QY 274 PKYMWSPSGPIHVPKNGILKGDTCNNMWIPDVGSTWMPKTPYIPPIITNRPTSKPTT 333
DB 262 PENSVK-----EVLAPGTI-----KDRIKKLLAHKNSMKKKA 294
QY 334 R---PTPKPTPIPTPPPTPLTELTPPTTPTTGLTTIAPAASTPPG----- 383
DB 295 KINKVTPEPTPTTP-----KVNLOPFNYEE-----IVSRGNSHGKKGKNEEK 338
QY 384 ---GITVDNRVQ-----TDQPKRGDVFIPQPSNDLFEIPEIRGVSADEAKDDPGV 434
DB 339 MKGCLDEKREKALANDIEERSLRGDVFPKVNAGEFGLILVQKALTSKLEHDKIAMI 398
QY 435 LVHSCNFDHGLCQWIREKNDLHWEP1-RDPAGGYLTVSAAKAPGGAARLVLPGLRLM 493
DB 399 SV-DCSFNHCIDKQDREDDFDWADPDRDNAIGFYMAVPALAGHKDTCRIKLLPDQ 457

QY 494 HSGDCLSLFRHKVTGLHSGTLOVFRKKAHCAALWGRNGHG--WROQTITL-RCAD-I 549
DB 458 POSNFCLLFDYRLAGDKVCKLRFVFK--NSNNALAWKTTSEDEKWKTKIOLYQGTDTAT 515
QY 550 KSVVFKEKRRGHTGEIGLDDVSLKKGHCSE 580
DB 516 KSLIFEAEKRGKTKGTAIVDGVLLVSGICPD 546
RESULT 5
US-09-363-316B-18
; Sequence 18, Application US/09363316H
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316H
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (501-502)
; OTHER INFORMATION: Xaa - any amino acid
US-09-363-316B-18

Query Match 31.7%; Score 1041.5; DB 4; Length 502;
Best Local Similarity 37.5%; Pred. No. 1e-64;
Matches 209; Conservative 92; Mismatches 170; Indels 87; Gaps 14;
QY 47 GWARQSGOCOPFYVLRQRIARCQLKAVCPCKKHGBCIGNKCKHPGVAGTKCIQV 106
DB 1 CWRNSKGVCF-----ATCEPCCKFGEVCGVGNKCRFPYGTCTSQD 43
QY 107 INECGLKPRCKHRCMNTGYSKYCLNGYMLMPOGSSSALTCSMANCOYCDVYKQGI 166
DB 44 VNECGMKPRPCQHRVCNTHGSKYKFCCLSGHMLMPDTCVNSRTCAMINCOYSCDETEEGP 103
QY 167 RCOCPSPGLQAPDGRTCVDVDECATGRASCPFRFCVNTFGSYCKCKHGFDMYLGCK 226
DB 104 QCLCPSSGURLAPNGRDCLDIDECASGKVICPYNRRVCNTEFGSYCKHIGFELYISGR 163
QY 227 YOCHDIDKCSIGQYQCSFARCYNVRGSKYCKCKEYQGGDGLTCVYIPKVMIEPSGPIHV 286
DB 164 YDCIDINECTMDSHTCSHHANCNTQGSFKCKCKQYKGNGLKCSALPENSVK-----KV 218
QY 287 PKNGNTILKGDTCNNMWIPDVGSTWMPKTPYIPPIITNRPTSKPTT---PTPKPTTP 343
DB 219 LRAPGTI-----KDRIKKLLAHKNSMKKKAIIKNTVPTPT 256
QY 344 TTPPPPTPLTELTPPTTPTTPTTGLTTIAPAASTPPG-----GITVDNRVQ- 392
DB 257 TP-----KVNLOPFNYEE-----IVSRGNSHGKKGKNEEKKEGLEDEKREK 300
QY 393 -----TDQPKRGDVFIPQPSNDLFEIPEIRGVSADEAKDDPGVLVHSCNFOHGLCG 447
DB 301 ALKNDIEERSLRGDVFPKVNAGEFGLILVQKALTSKLEHDKIAMI-SV-DCSFNHCID 359
QY 448 WIREKNDLHWEP1-RDPAGGYLTVSAAKAPGGAARLVLPGLRLMHSGLCLSLFRHKV 506
DB 360 WKQDREDDFDWADPDRDNAIGFYMAVPALAGHKDIGRLKLLPDQPOSNECLLFDYSL 419
QY 507 TGIHSGTLOVFRKKAHCAALWGRNGHG--WROQTITL-RCAD-IKSVVFKGKRRGH 562

Search completed: April 23, 2003, 13:04:12
Job time : 33 secs